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new U.S. Patent 5,981,839,

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08/812,665, filed March 7, 1997, which is a

In the Claims

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17. (Amended) A method for obtaining a plant having a modified phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in plant seed tissue, a DNA sequence of interest other than the native coding sequence of said gene, and transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell, regenerating a plant from said transformed plant cell, and growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said modified phenotype is obtained.

18. (Amended) A method of altering the phenotype of plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant seed tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

19. (Reiterated) The method according to Claim 17 or 18, wherein said DNA construct is flanked by T-DNA.

20. (Reiterated) The method according to Claim 19, wherein said plant is soybean or

rapeseed plant.

21. (Reiterated) The method according to Claim 17 or 18 wherein said DNA sequence of interest encodes an enzyme.

22. (Reiterated) The method according to Claim 17 or 18 wherein said DNA sequence of interest is an antisense sequence.

23. (Reiterated) The method according to Claim 17 or 18 wherein said gene is transcribed during seed embryogenesis.

24. (Reiterated) The method according to Claim 23 wherein said gene is transcribed from about day 7 to day 40 postanthesis.

25. (Reiterated) The method according to Claim 17 or 18 wherein said gene is transcribed during seed maturation.

26. (Reiterated) The method according to Claim 25 wherein said gene is transcribed about day 11 to day 30 postanthesis.

27. (Reiterated) The method according to Claim 18, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

28. (Reiterated) A method for modifying a genotype of a plant to impart a desired characteristic to seed as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein said transcription of said gene is regulated in a plant seed tissue, a DNA sequence of interest other than the native coding sequence of said gene, and a transcriptional

termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and
growing said plant to produce seed having a modified genotype.

29. (Reiterated) The method according to Claim 28, wherein said DNA construct is flanked by T-DNA.

30. (Reiterated) The method according to Claim 28, wherein said plant is a *Brassica* plant.

31. (Reiterated) The method according to Claim 28, wherein said DNA sequence of interest encodes an enzyme.

32. (Reiterated) The method according to Claim 28, wherein said DNA sequence of interest is an antisense sequence.

33. (Reiterated) The method according to Claim 28, wherein said plant is a soybean plant.

34. (Reiterated) A method for modifying transcription in seed tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing seed tissue under conditions to produce seed, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a seed-specific transcriptional initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said seed-specific transcriptional initiation region.

35. (Reiterated) The method according to Claim 34, wherein said DNA sequence of interest is an antisense sequence.

36. The method according to Claim 34, wherein said plant is of the genus *Brassica*.

37. (Reiterated) The method according to Claim 34, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

38. (Reiterated) The method according to Claim 34, wherein said plant is a soybean plant.

39. (Reiterated) A method to selectively express a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a seed tissue under conditions to produce seed, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a seed-specific transcriptional initiation region and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said seed-specific transcriptional and translational initiation region.

40. (Reiterated) The method according to Claim 39, wherein said plant is of the genus *Brassica*.

41. (Reiterated) The method according to Claim 39, wherein said plant is a soybean plant.

Add the following new claims:

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42. (New) A method according to Claim 17 or Claim 18, wherein said gene is selected from the group consisting of a napin gene, ACP gene, cruciferin gene, or EA9 gene.

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43. (New) The method according to Claim ¹17 or Claim ²18, wherein said DNA sequence of interest is a structural gene.

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44. (New) The method according to Claim ¹17 or Claim ²18, wherein said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

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45. (New) The method according to Claim ¹17 or Claim ²18, wherein said transcriptional initiation region further comprises a translational initiation region.

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46. (New) A method for modifying transcription in plant seed tissue as distinct from other plant tissue, said method comprising growing a plant wherein said plant comprises cells containing a DNA construct integrated into their genome, said construct comprising:

regulatory region from a gene wherein said gene is expressed in plant seed tissue, a DNA sequence of interest other than the coding sequence native to said regulatory regions, whereby said DNA sequence of interest is expressed under control of said regulatory regions.

47. (New) The method according to Claim 47, wherein said regulatory region comprise transcriptional and translational initiation and termination regions.

48. (New) A method to selectively express a heterologous DNA sequence of interest in plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant wherein said plant comprises cells containing a DNA construct integrated into their genome, said construct comprising a tissue specific expression cassette and a DNA sequence of interest, wherein said DNA sequence of interest is expressed under the control of said tissue specific expression cassette whereby said DNA sequence of interest is expressed in plant seed tissue.